

Result No.	Score	Query Match Length	DB ID	Description	Summaries
c 1	261.2	54.0	520	C14748 Clontech human aorta polyA+ mRNA (#6572) Homo sapiens cDNA	1. (bases 1 to 520)
c 2	260.6	53.9	699	AQ990151 Rfc00973	Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M., Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shiromizu, H., Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y., Maekawa, H., Shin, S., and Nakamura, Y.
c 3	225.4	46.6	464	D80872 HOM113A12A	Fujiwara et al. (1995)
c 4	186.4	38.5	593	BZ351818 hx72905.g	Unpublished (1995)

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OM nucleic - nucleic search, using sw model

Run on: June 15, 2004, 09:22:37 ; Search time 2144.55 Seconds (without alignments)

Title: US-09-973-674A-16

Perfect score: 484

Sequence: 1 atgcgaattggacacggtt.....taaggcaacaatgttga 484

Scoring table: IDENTITY_NUC Gapop 10_0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : EST:*

- 1: em_estba:*
- 2: em_estnum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estsom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_p1n:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_pig:*
- 27: em_gss_vz1:*
- 28: gb_gss1:*
- 29: gb_gss2:*

RESULT 1
C14748/C

LOCUS C14748 Clontech human aorta polyA+ mRNA EST 30-SEP-1996

DEFINITION clone GEN-086902 3', mRNA sequence.

ACCESSION C14748

VERSION C14748.1 GI:1569455

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE Fujiwara, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, M., Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shiromizu, H., Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y., Maekawa, H., Shin, S., and Nakamura, Y.

AUTHORS Fujiwara et al. (1995)

COMMENT Contact: Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharma International Co., Ltd
463-10 kagasuno Kawachi-cho, Tokushima, 771-01 Japan
Tel: 0886-65-2888
Fax: 0886-37-1035.

FEATURES Location/Qualifiers
Source 1. . 520 bp mRNA mRNA
SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:3606"
/clone_id="GEN_086B02"
/clone_lib="Clontech human aorta polyA+ mRNA (#6572)"

ORIGIN

Query Match	Score	Length	DB	28;	Length	699;	ORIGIN
Best Local Similarity	54.0%	520;	Pred. No.	4	Gaps	3;	
Matches	295;	Conservative	Pred. No.	4.7e-59;	Indels	4;	
Qy	171	GGCAAGCTTCCGGATACCGATCGGATTAAAGTGCCGATAGCGCAGGTGGT	230				
Db	520	GGCAAGCTTCCG-ATGCCATASCGGACGCB-T	465				
Qy	231	ACGGGAGGCTGGCTGGTATTCAAGGAGGTATAACCTTGCAACGTCATGTCAC	290				
Qy	464	ACSGAAAGCCGCGTGCATTCAGCGRGTTAACCTTGGCAAGTCGATGTCAC	405				
Qy	291	TATCATCGCTCAGGGCACAGGATGTTGCCACATTCCACAAATGCCGTGTTATTGC	350				
Db	404	TATCATCGCTCAGGACGGATGTTGCCACATTCCACAAATGCCGTGTTATTGC	345				
Qy	351	CGAAGATTCGCTGCCATTGGATCATGGATCATGTTAACGTGAAGCCACTACTACGGAAAAACT	410				
Db	344	CGAAGATTCGCTGCCATTGGATCATGGATCATGTTAACGTGAAGCCACTACTACGGAAAAACT	285				
Qy	411	GGGATTACCGACGTGGAGGGATTGCTGTGAAGCGCTGGCTACTCATTAAGGC	470				
Db	284	GGGATTACCGACGTGGCTGCAATTGGATCATGTTAACGTGAAGCCACTACTACGG	225				
Qy	471	AACAAATGATTGA	484				
Db	224	AACAAATGATTGA	211				

RESULT 2

AQ990151 699 bp DNA linear GSS 14-AUG-2000
LOCUS Rfcl0873 Photorhabdus luminescens strain W14 M13 library
DEFINITION Photorhabdus luminescens genomic clone PLG00873, genomic survey sequence.
ACCESSION AQ990151
KEYWORDS AQ990151..1 GI:9648745
SOURCE GSS
ORGANISM Photorhabdus luminescens
BACTERIA Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
REFERENCE ffrench-Constant, R.H., Waterfield,N., Burland,V., Perna,N.T.,
AUTHORS Daborn,P.J., Bowen,D. and Blattner,F.R.
TITLE A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
JOURNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
MEDLINE 20378633
PUBMED 10919786
COMMENT Contact: ffrench-constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826521
Fax: (44) 1225 826779
Email: bsurfco@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) Please see ffrench-Constant et al. 2000, Nucleic
Acids Res. M13 Forward

FEATURES

source

Class: shotgun
Location/Qualifiers

1.. 699
/organism='Photorhabdus luminescens'

/mol_type="genomic DNA"
/strain="W14"
/db_xref="taxon:29488"
/ciLine="PLG00873"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13 library"
/library"
/NOTE="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Jamus."

Query Match	Score	Length	DB	28;	Length	699;	ORIGIN
Best Local Similarity	53.8%	520;	Pred. No.	7.5e-59;	Indels	1;	
Matches	346;	Conservative	Pred. No.	7.5e-59;	Indels	1;	
Qy	1	ATGCCATGGACGGTTTGACCTACATGCCCTTGGCGTGAAGGCCAATTTATCATT	60				
Db	19	ATGAGCATGGACGGTTTGACATTAATTGGTGTGAGGGCGATTTATT	78				
Qy	61	GTTGGGTAGCATCTTACGAAAGATGTTGGCGCATTCATGGGACCTGGG	120				
Db	79	GTTGGTGTGTTGTTATCTGATGGTGTATTTGCTGATTTGCT	138				
Qy	121	CCTCATGCGTGAACCGATGTTGGCGATGTTGGCGTGGGATATGGPAGCTG	180				
Db	139	CTCCAGATCTGGCCACCGATGTTGTTAGGTCTGGCATGGTGTATGGGAAATT	258				
Qy	181	TTCCCGGATACCGATCCGGCATTTAAGGTCGCCGAGCTGCTACGCCAGCC	240				
Db	199	TTCCCGGATCTGGCCACCGATGTTGTTAGGTCTGGCATGGTGTATGGGAAAGCC	258				
Qy	241	TGGCTTCGTTATTCAAGGCTTATACCTTGCAACCGTCACTATCATCGCT	300				
Db	259	TATTACGTATCAGGAAACGGTTATGGATGTTGGAAATTCTGGATCTGCT	318				
Qy	301	CAGGACCGAGATGTTGCCACATTCCAAATGCGCTGTTATTGGCGAAGATCTC	360				
Db	319	CAAGGACCCAAATTGTGCCCATATTCCAACAAATGAGCTCAATCTGGCGAAGATCT	378				

RESULT 3

D80872/C 464 bp mRNA linear EST 09-FEB-1996
LOCUS HOM113A12A Human fetal brain (rFujiwara) Homo sapiens cDNA clone
DEFINITION DEFINITION GEN-113A12 3', mRNA sequence.

AUTHORS Fujiwara,T., Hirano,H., Katadiri,T., Kawai,A., Kuga,Y., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimaeda,Y., Shinomiya,H., Takahashi,E., Hirai,Y., Maekawa,H., Shin,S. and Nakamura,Y.

ACCESSION D80872
KEYWORDS D80872/1 GI:1178749
VERSIONS EST.
KEYWORDS SOURCE
ORGANISM Homo sapiens (human)
DEFINITION Homo sapiens
DEFINITION Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
DEFINITION Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
DEFINITION 1 (bases 1 to 464)
DEFINITION HOM-113A12 3', mRNA sequence.

TITLE TITLE
JOURNAL JOURNAL
COMMENT COMMENT

Otsuka GEN Research Institute
Otsuka Pharmaceutical Co.,Ltd
463-10 kagasuno Kawauchi-cho, Tokushima, 771-01 Japan
Tel: 0886-65-8888
Fax: 0886-37-1035.

FEATURES	Location/Qualifiers
source	1..464 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="GEN-113A12" /dev_stage="fetal" /clone_lib="human fetal brain (Fujiwara)" /note="Organ: brain"
ORIGIN	Query Match 46 6%; Score 225 4; DB 14; Length 464; Best Local Similarity 97.2%; Pred. No. 1.7e-49; Matches 246; Conservative 4; Mismatches 1; Indels 2; Gaps 2;
QY	233 GCGAACCTGGCTGGTGTATCAGGGAAAGGGTTAACCCCTGGCACCTGGTGTACTA 292
Db	464 SCGAAGCCTGGCTGGBCTATTAGGGCAARSGCTTAAACCCCTGGCACCTGGTGTACTA 405
QY	293 TCACTGCTAGGACCGAAATGTTGCGGA-CATTCCACAAATGCCGTGTATTGCC 351
Db	404 TCATGCTCA-GCACCGAAGATGTTGCCATCATTCACWAATGCGGTGTTATGCC 346
QY	352 GAAGATCTGGCTGGCATATGGATGATGTTAACCTGAAAGCCACTACTAGGAAAAACTG 411
Db	345 GAAGATCAGCTGCCATTAGGATGATGTTAACGTGAAAGCCACTACTAGGAAAAACTG 286
QY	412 GGATTTACCGAACCTGGGGAGGGATTGCTGTGAGGGCTGGCTACTCATTAAGGA 471
Db	285 GGATTTACCGAACCTGGGGAGGGATTGCTGTGAGGGCTGGCTACTCATTAAGGA 226
QY	472 ACAAAATGATTGA 484
Db	225 ACAAAATGATTGA 213

RESULT 4	LOCUS	DEFINITION	VERSION	KEYWORDS	ORGANISM	REFERENCE	TITLE	JOURNAL	COMMENT
B2351818/c	B2351818	bz72905_91 WGS-SbicolorF (JM107 adapted methyl filtered) Sorghum bicolor genomic clone hx72905 5', Genomic survey sequence.	GI:24915450	GSS	Sorghum bicolor (sorghum)	Rabinowicz,P.D., O'Shaughnessy,A.L., Balija,V., Dedhia,N., Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L., Zutavern,T., Palmer,L., McCombie,W.R. and Martienssen,R.A. Unpublished (2002)	Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA Tel: 516 367 8884 Fax: 516 367 8874 Email: mccombie@cshl.org Seq primer: -21M13uniRev Class: shotgun High quality sequence stop: 593. Location/Qualifiers	Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA Tel: 516 367 8884 Fax: 516 367 8874 Email: mccombie@cshl.org Seq primer: -21M13uniRev Class: shotgun High quality sequence stop: 593. Location/Qualifiers	

FEATURES	source
	1..593 /organism="Sorghum bicolor" /mol_type="genomic DNA" /db_xref="taxon:4558" /clone="hx72905" /lab_host="JM107 or DH5a"
	1..594 /organism="Sorghum bicolor" /mol_type="genomic DNA" /db_xref="taxon:4558" /clone="id51c09" /lab_host="DH5a"

/clone.lib="WGS-SbicolorPF (DH5a methyl filtered)"
 /note="Site 1: Xba I; Site 2: Xba I; The vector was digested with Xba I and one nucleotide was added by fill in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments and size were between 0.8 and 3 kb and were cloned into the vector (.xly reads in M1mp19, .b/g reads in pUC19). The same ligation was transformed into DH5a."

ORIGIN

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Query Match          38.1%;  Score 184.4;  DB 28;  Length 654;
Best Local Similarity 80.8%;  Pred. No. 1.8e-38;
Matches 215;  Conservative 0;  Mismatches 51;  Indels 0;  Gaps 0;
Qy   1 ATGGGATTTGGACACCGTTTGACGTACATGCCTTGGGGATAATTCAATT 60
Db   382 ATGGPATCGGTACGGTTACGGTTACGGTACGGGAGCGTTGGTGTGATT 441
Qy   61 GSTGGCSTACGGATTCCTACGAAAGGATGCTGCGCATTCGATGGGACGTGGC 120
Db   442 GCGGGTGGPATTCCTACAGCTTATGCAITCCAGGGCATGTGGC 501
Qy   121 CTCCATGCTGTTACCGATGCTTGCCTGGGATATCGCAAGCTG 180
Db   502 CTGCATCGCTGCTAACCGAGCGCTGCTGGCGTGGCATGGCACATCGCAAATG 561
Qy   181 TTCCCGATACGGATCCGCAATTAAAGTGGCATAGCCGGAGCTGCTACGGGAAGCC 240
Db   562 TTCCGGAAACCGATCGGCATTAAGGGCGGATGCGGAGCTGCTGGCGAAGCC 621
Qy   241 TGGCGTCCTATTAGGGAAAGGTTA 266
Db   622 TGGCGTCCTATTAGGGAAAGGCTA 647

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RESULT 6

BZ567684 BZ567684 1350 bp DNA linear GSS 17-DEC-2002
 DEFINITION pacS2-164_7159_x1 pacS2-164 Pseudomonas aeruginosa genomic clone
 ACCESSION BZ567684
 VERSION 1
 KEYWORDS
 SOURCE Pseudomonas aeruginosa
 ORGANISM Pseudomonadaceae; Pseudomonas
 Pseudomonas aeruginosa library
 REFERENCE Spencer,D.H., Raymond,C.K., Smith,B.E., Sims,E.B., Hastings,M.,
 Burns,J.L., Kaul,R. and Olsen,M.V.
 TITLE Whole-Genome-Sequence variation among multiple isolates of
 JOURNAL Pseudomonas aeruginosa
 COMMENT Contact: Chris K. Raymond
 Genome Center Washington University
 Box 352145, Seattle, WA 98105-2145, USA
 Tel: 2062216954
 Fax: 2066557244
 Email: raymond@u.washington.edu
 Class: shotgun
 Location/Qualifiers

FEATURES

source 1_1350
 /organism="Pseudomonas aeruginosa"
 /mol_type="genomic DNA"
 /strain="2_164"
 /db_xref="txon:287"
 /clone="pacS2-164_7159"
 /clone.lib="pacS2-164_7159"
 /note="Clinical isolate 2-164 Whole genomic shotgun library."
 ORIGIN

Query Match 28.6%; Score 138.4; DB 28; Length 1350;
 Best Local Similarity 58.0%; Pred. No. 4.7e-26;
 Matches 244; Conservative 0; Mismatches 177; Indels 0; Gaps 0;
 Qy 1 ATGGGATTTGGACACCGTTTGACGTACATGCCTTGGGGATAATTCAATT 60
 Db 174 ATGAAACTCGGCATGGTTACCGTCATGGCTGGGAACTGATCACCCCT 233
 Qy 61 GTGGGGTACCGATTCCTAGAAAGGATTGGCATTCGATGGGACGGCGC 120
 Db 234 GCGGAGTGGGATGGCATGGCCAAACATGGGTGGGCCACTCTACGGGAGCTG 293
 Qy 121 CTCCATGCTGTTACGGCATTCGCTGGGGATAATGGCAAGCTG 180
 Db 294 CTGGCAGGCCCTGTCGATGGGGATCTCGCGCACATCTTCAGCAC 353
 Qy 181 TTCCCGATACGGATCCGCAATTAAAGTGGCATAGCCGGAGCTGTAAGGGAGCC 240
 Db 354 TCTCGGACACGGACCGAACCGTGGTCAAGGCTCCTACAGTCGGCGTGGGACAGTG 413
 Qy 241 TGGCGTCCTATTAGGGAAAGGTTA 300
 Db 414 ATCGGCATCGTGGGAGCCCTGCGTGAAGGGTGGCATCTGGTGTGTC 473
 Qy 301 CAGGACACGGAAATGTTGGCCACATTCCAAATGGCGTGTATTGGCGAAAGATCTC 360
 Db 474 CATGGCAGAAATGGCTGGCCACATGAGAACATGCGCAAGGA-CAT 533
 Qy 361 GGTTGCCATATGGATGATGTTAACGTTAACGCAACTACGGATTTACC 420
 Db 534 TGGCTNTTGAGCATGGCTGAGCTGCTGGCCACCATTCGAGGAGCTGTATTAAACC 593
 Qy 421 G 421
 Db 594 G 594

RESULT 7

AQ991620 AQ991620 800 bp DNA linear GSS 14-AUG-2000
 LOCUS Rfc01133F Photorhabdus luminescens strain W14_M13 library
 DEFINITION Photorhabdus luminescens genomic clone PLG01133F. Genomic Survey
 GSS. sequence.
 ACCESSION AQ991620
 VERSION 1 (bases 1 to 800)
 KEYWORDS GSS
 SOURCE Photorhabdus luminescens
 ORGANISM Photorhabdus luminescens
 Pseudomonadaceae; Photorhabdus; Enterobacteriales;
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Photorhabdus.
 AUTHORS ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
 Daborn,P.J., Bowen,D., and Blattner,F.R.
 TITLE A genomic sample sequence of the entomopathogenic bacterium
 Photorhabdus luminescens W14: Potential implications for virulence
 Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
 JOURNAL 20378633
 MEDLINE 10919786
 PUBMED
 COMMENT Contact: ffrench-Constant RH
 Department of Biology and Biochemistry
 University of Bath
 South Building, Bath BA2 7AY, UK
 Tel: (44) 1225 826621
 Fax: (44) 1225 826779
 Email: bssrfc@bath.ac.uk
 This is one of a selected subset of flipped clones from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al.
 2000, Nucleic Acids Res.
 Seq. Primer: M13 Reverse
 Class: shotgun
 Location/Qualifiers

ORIGIN		1..800 /organism="Photorhabdus luminescens" /mol_type="genomic DNA" /strain="W14" /db_xref="taxon:29488" /clone="PfG0113F" /dev_stage="primary phase variant" /clone_lib="photorhabdus luminescens strain W14 M13 library" /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."	Best Local Similarity 95.6%; Pred. No. 1.7e-23; Matches 151; Conservative 2; Mismatches 2; Indels 3; Gaps 2; Score 137; DB 28; Length 800;
Query Match	28.3%;		
Best Local Similarity 70.4%; Pred. No. 9.1e-26;	Length 800;		
Matches 182; Conservative 0; Mismatches 76; Indels 0; Gaps 0;			
Qy	214 GATAGCCGGACCTGCTTACCGCAAGGCTGGCTCGTATTAGGGTTATAACCTCT 273	RESULT 9 AQ242254	
Db	30 GATAGCGTAATTATTGCGCAAGCTTATTACGTATANAAAAGGGTTATCGGATT 89	LOCUS DEFINITION	AQ242254 577 bp DNA linear Ochrobactrum anthropi GSS 31-AUG-2001
Qy	274 GGCAACTCGAAGTCACTATCATGCTCAGGCCACCCAAAGTGTGGCGCACATTCCAA 333	ACCESSION	3P02-39r: Ochrobactrum anthropi BAC Library Ochrobactrum anthropi genomic clone 3P02-39r, genomic survey sequence.
Db	90 GGCAATTGGAATTAGGATTATCGCTCAAGCACCRAAAATGCTGCCATTCCCAA 149	VERSION	AQ242254.1 GI:3688053
Qy	334 ATGGCGCTTTATTGCCGAGATCTGGCTGCCATATGGATGTTAACGTGAAAGCC 393	SOURCE	GSS
Db	150 ATGAGAGTCATCTGCAGAGATCTACAATGCCACATTGATGATCATCATGTTAACGC 209	ORGANISM	Ochrobactrum anthropi
Qy	394 ACTACTACGGAAAAACTGGGATTACGGAGCTGGGGAAAGGGATTGCCCTGTGAAGCGGTG 453	REFERENCE	Brucellaceae; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Db	210 ACAACTACCGAGAAAATTAGGATTGTTGGCTTAAGAAGGGATTATGGCTGGAAAGCAGT 269	AUTHORS	Tomkins,J.J., Miller-Smith,H., Sasinowska,M., Choi,W., Sasinowska,H., Verce,M., Freedman,D., Dean,R. and Wing,R.A.
Qy	454 GCGCTACTTAAAGCCA 471	TITLE	Physical map and gene survey of the Ochrobactrum anthropi genome using bacterial artificial chromosome contigs
Db	270 GCTTGCTGGTAAGGAA 287	JOURNAL	Microb. Comp. Genomics 4 (3), 203-217 (1999)
		MEDLINE	20052529
		PUBMED	10587947
		COMMENT	Contact: Wing RA
			Clemson University Genomics Institute
			100 Jordan Hall, Clemson, SC 29634, USA
			1. (bases 1 to 577)
			REFERENCE
			AUTHORS
			Tomkins,J.J., Miller-Smith,H., Sasinowska,M., Choi,W., Sasinowska,H., Verce,M., Freedman,D., Dean,R. and Wing,R.A.
			VERSION
			1.0
			KEYWORDS
			Ochrobactrum anthropi
			Bacteria; Proteobacteria; Ochrobactrum.
			FEATURES
			1..577
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			/organism="Ochrobactrum anthropi"
			/mol_type="genomic DNA"
			/db_xref="Taxon:29"
			/clone="3P02-39r"
			/lab_host="DH10B E. coli"
			/clone_lab="Ochrobactrum anthropi BAC Library"
			/note=Vector: pBelobBAC11; Site: HindIII; Site 2: HindIII; Ochrobactrum anthropi is an important microbe having potential for the bioremediation of environments contaminated by aliphatic compounds. We have constructed a BAC library for O. anthropi that provides a 90x genome coverage based on an estimated genome size of 3.83 Mb. The library contains 3072 clones with an average insert size of 112 kbp. High-density colony filters of the library were made and a physical map of the genome constructed using a hybridization without replacement strategy. In addition, 624 randomly chosen BAC clones were HindIII fingerprinted and analyzed using Fingerprint Contig (FPC; Sangre Centre, UK). The FPC results closely supported and verified the hybridization contig data.
			After determining a reduced tiling path of 69 clones, 138 BAC ends were sequenced for a genome wide survey of gene distribution and gene structure."
			ORIGIN
			Query Match 26.4%; Score 128; DB 13; Length 370;

```

Best Local Similarity 54.5%; Pred. No. 5.4e-23;
Matches 253; Conservative 0; Mismatches 211; Indels 0; Gaps 0;
Query 1 ATGGAAATGGACCGTTTACGTAATGCCATTGCTTGGGGAAAGCCATTATCAT 60
Db 65 ATTGTACTGGAAATGTTACGTCATCCTTGAAACGGCATCTGGCTG 124
Qy 61 GGTGGCTACGGATTCTTACGAAAAAGGATGCTGGCACCTCTGATGGCACGGTGGC 120
Db 125 TCGGGTGAATACTCCACAAAGCAACATGGCAATGCGCATGTGGA 184
Qy 121 CTCCATGGTACCGATGCTATGGCTGGGGATATCGGAAGCTG 180
Db 185 CTTCATGGTACGACTAACGGCCCTGCTGCGACGGGATATCGGACCAT 244
Qy 181 TTCCGGATACCGATGGCATTAAAGTGCCTGGGATAGCGGAGCTAGCGGAAGCC 240
Db 245 TTCCCGCTTCCACCC2CANTGAAGGGCTGCTCCGATCTGGACATGCT 304
Qy 241 TGGCGTCTTTCAGGGAAAGGGTTATACCTTGGCAACGTGATGACTATCGCT 300
Db 305 GCAAATATGGGGTGAAGCTGGCATGTCACGTGACCTTATAGC 364
Qy 301 CAGGCACCGAAGATGTTGCCGAGATTCACAAATGCCGAGATCTC 360
Db 365 GAAGCACGAAGATGCCCAATGCGCATGTCAGCTTGTGACATGGTG 424
Qy 361 GGCTGCCATATGGATGTTAACGTGAAAGCCACTAACGGAAAAMCTGGATTAACC 420
Db 425 GAAATTGGCCGATGGGTTCCATCAAGGACAAATGAAAGCTGGCTTCCTC 484
Qy 421 GGACGTGGGAAAGGATTGGCTTGTGAAAGGGTGGCTACTCAT 464
Db 485 GGACGCCGTAAGGTATGCTGCCATTGCAACGGCAACCGTCAT 528

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RESULT 1.0
LOCUS BF633873/C
DEFINITION NF072A05DTIPI036 Drought Medicago truncatula cDNA clone NF072A05DT
ACCESSION BF633873
VERSION BF633873.1
KEYWORDS EST
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
COMMENT 1 (bases 1 to 305)
The Samuel Roberts Noble Foundation
Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
Flores,H.R., Imman,J.T., Weller,J.W. and May,G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Unpublished (2000)
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 305 Std Error: 0.00
Plate: 074 row: G column: 12
Seq primer: TCACACAGGAAACGCTTGTGAC.
Location/Qualifiers
1..305 /organism="Medicago truncatula"
/mol_type="mRNA"
/db_xref="taxon:3880"
/clone="NF072A05DT"
/tissue_type="plantlets"
/dev_stage="pooled_timepoints"
/clone.lib="Drought"
/note="Vector: Lambda Zap; Contains a mixture of entire
plantlets harvested in a series of days-post-watering
timepoints."

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ORIGIN
Query Match 25.4%; Score 123; DB 10; Length 305;
Best Local Similarity 100.0%; Pred. No. 3.4e-22;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Query 362 GCTGCCATATGGATGTTAACGTGAAAGCCACTACTACGGAAAAGCCATTACCG 421
Db 305 GCTGCCATATGGATGTTAACGTGAAAGCCACTACTACGGAAAAGCCATTACCG 246
Qy 422 GACGTGGGAAAGGGATGGCTGGCTACTCATTAAGGCAACAAATGAT 481
Db 245 GACGTGGGAAAGGGATGGCTGGCTACTCATTAAGGCAACAAATGAT 186
Qy 482 TGA 484
Db 185 TGA 183

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RESULT 1.1
LOCUS BF634326/C
DEFINITION 5' mRNA sequence.
ACCESSION BF634326
VERSION BF634326.1
KEYWORDS EST
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
COMMENT 1 (bases 1 to 305)
The Samuel Roberts Noble Foundation
Torrez-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
Flores,H.R., Imman,J.T., Weller,J.W. and May,G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Unpublished (2000)
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble.org
Insert Length: 305 Std Error: 0.00
Plate: 074 row: G column: 12
Seq primer: TCACACAGGAAACGCTTGTGAC.
Location/Qualifiers
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/clone="NF074G12DTIPI039"
/tissue_type="plantlets"
/dev_stage="pooled_timepoints"
/clone.lib="Drought"
/note="Vector: Lambda Zap; Contains a mixture of entire
plantlets harvested in a series of days-post-watering
timepoints."

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ORIGIN
Query Match 25.4%; Score 123; DB 10; Length 305;
Best Local Similarity 100.0%; Pred. No. 3.4e-22;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Query 362 GCTGCCATATGGATGTTAACGTGAAAGCCACTACTACGGAAAAGCCATTACCG 421

```


Box 352145, Seattle, WA 98105-2145, USA
 Tel: 2022165954
 Fax: 206857244
 Email: craymond@u.washington.edu
 Class: shotgun.
FEATURES
 source Location/Qualifiers
 1..811 /organism="Pseudomonas aeruginosa"
 /mol_type="genomic DNA"
 /strain="MSH"
 /db_xref="MSH"
 /clone="msh2_5245"
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 /note="Environmental isolate. Whole genomic shotgun library."

ORIGIN

	Query	Match	Score	Length	DB	28;	Length	811;	
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Local	Qy	ATGGGATTGACACCGTTGACTAACGCTTGGGTGAAGCCATTATCAT	59.7%	5.9e-21;	Pred.	No.	5.9e-21;		
Similarity	Qy	ATGGGATTGACACCGTTGACTAACGCTTGGGTGAAGCCATTATCAT	0;	Mismatches	0;	Indels	0;	Gaps	0;
Matches	Db	ATGGGATTGACACCGTTGACTAACGCTTGGGTGAAGCCATTATCAT	200	441	ATGGGATTGACACCGTTGACTAACGCTTGGGTGAAGCCATTATCAT	500			
200;	Qy	ATGGGATTGACACCGTTGACTAACGCTTGGGTGAAGCCATTATCAT	60	61	ATGGGATTGACACCGTTGACTAACGCTTGGGTGAAGCCATTATCAT	120			
Conservative	Db	ATGGGATTGACACCGTTGACTAACGCTTGGGTGAAGCCATTATCAT	560	501	ATGGGATTGACACCGTTGACTAACGCTTGGGTGAAGCCATTATCAT	560			
0;	Qy	ATGGGATTGACACCGTTGACTAACGCTTGGGTGAAGCCATTATCAT	560	121	ATGGGATTGACACCGTTGACTAACGCTTGGGTGAAGCCATTATCAT	180			
0;	Db	ATGGGATTGACACCGTTGACTAACGCTTGGGTGAAGCCATTATCAT	620	561	ATGGGATTGACACCGTTGACTAACGCTTGGGTGAAGCCATTATCAT	620			
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Search completed: June 16, 2004, 06:30:13
 Job time : 2152.75 secs

